## 1/9

## Nucleotide Sequence of First Rhesus HER2/Neu

1 ATGGAGCTGG CGGCCTGGTA CCGCTGGGGG CTCCTCCTGG CCCTCTTGCC CAGTCCCGAG 61 GCGGGCACCC AAGTGTGCAC CGGCACAGAC ATGAAGCTGC 61 GCGGGCACCC AAGTGCTCCG CCACCTCTAC CAGGGCTGCC AGGTGCTCA CAGTCCCGAG 121 ACCCACCTGG ACATGCCCAC CAATGCCAGC CTCTCCTTCC GCAGGATAT CCAGGAGGTG 181 GAACTCACCT ACCTGCCCAC CAATGCCAGC CTCTCCTTCC TGCAGGATAT CCAGGAGGTG 181 GAACTCACCT ACCTGCCCAC CAATGCCAGA GTGAGGCAGG TCCCACTGCA GAGGCTGCGG 182 CAGGGCTACG TGCTCATCGC TCACAACCAA GTGAGGCAGG TCCCACTGCA GAGGCTGCGG 183 ATTGTGCGAG GCACCCAGCT CTTTGAGGAC AACTATGCCC TGGCCGTGCT AGACAATGGA 182 CAGCTTGGAA GCACTACAGA GATCTTGAAA GGAGGGGCTT CGGCGGGCCT CCGGGAGGCTG 182 CAGCTTGGAA GCCTCACAGA GATCTTGAAA GGAGGGGCTT TGATCCAGCG GAACCCCCAG 183 CTCTCACACTGA TCGACACCAA CCGCTCTCGG GCCTGCCACC CCTGTTCTCC AGTGTGTAAA 183 CTCCACACTGA TGGACACCAA CCGCTCTCGG GCTTGCCACC CCTGTTCTCC AGTGTGTAAA 184 CTCACACTGA TGGACACCAA CCGCTTCTGAG GCTTGCCACC CCTGTTCTCC AGTGTGTAAA 185 GGCTCCCGGCT GCTGGGGAGA GAGTTCTGAG GCTTGCCACC CCTGTTCTCT AGTGTAAACAC 186 GCCTGCCGGCT GCTGGGGAGA GAGTTCTGAG GCTTGCCACC CTGCCCCCAC CCTTTCTTCTGT 186 GCCGGTGGCT GTGCCCGCTG CAAGGAGCCC CTGGCCACC ACTGCCCACC CTTCAACCAC 181 AGCGGCATCT GTGARCTGCA CTGCCCAGCC CTGGTCACCT ACACACACAA CACCTTTCAG 184 TCCATGCCCA ACCCCGAGGC CCGAGGTATACA TTCGGGCCCA GCTGTGTGAC TGCCCTCCC 181 ACAACTACC TTTCTACGGA CGTGGGATACA TTCGGGCCCA GCTGTGTGAC TGCCCTGCCC	_		0000070074	000070000	OTOCTCOTCO	CCCTCTTCCC	CCCCCCACCT
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361 GACCTGCTGA ACAATACCAC CCCTGTCACA GGGGCCTCCC CAGGAGGCCT GCGGGAGCTG 421 CAGCTTCGAA GCCTCACAGA GATCTTGAAA GGAGGGTCT TGATCCAGCG GAACCCCCAG 481 CTCTGCTACC AGGACACGAT TTTGTGGAAG GACTCTTCC ATAAGAACAA CCAGCTGGCT 541 CTCACACTGA TCGACACCAA CCGCTCTCGG GCCTGCCACC CCTGTTCTCC AGTGTGAAG 601 GGCTCCCGCT GCTGGGGAGA GAGTTCTGAG GATTGCAAA GCCTGCCCACC CCTGTTCTCC AGTGTGTAAG 601 GGCTCCCGCT GTGGCCGGCTG CAAGGGGCCA CTGCCCACTG ACTGCTCCCA TGAGCAGTT 721 GCTGCCGGCT GCACGGGCCC CAAGCACTCT GACTGCCCACTG ACTGCTCCCA TGAGCAGTT 721 GCTGCCGGCT GCACGGGCCC CAAGCACTCT GACTGCCCACTG ACTGCCCCCA CCTTCAACCAC 781 AGCGGCATCT GTGARCTGCA CTGCCCAGCC CTGGTCACC ACACCACAA 781 AGCGGCATCT GTGARCTGCA CTGCCCAGCC CTGGTCACC ACACACAAA 781 AGCGGCATCT GTGARCTGCA CTGCCCAGCC CTGGTCACC ACACACAAA 781 AGCGGCATCT GTGARCTGCA CTGCCCAGCC CTGGTCACC ACACACAAA 781 AGCGGCATCT GTGARCTGCA CTGCCCCAGCC CTGGTCACC ACACACAAA 781 AGCGGCAAC CCGGAGGACGG CGTGGGATCC TGCACCCCTC TCTGCCCCCT GCCCAACCCAA							
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1201 GAGACTCTGG AAGAGATCAC AGGTTACCTA TACATCTCAG CATGGCCAGA CAGCCTGCCT 1261 GACCTTAGCG TCCTCCAGAA CCTGCAAGTA ATCCGGGGAC GAATTCTGCA CAATGGCGCC 1321 TACTCACTGA CCCTGCAAGG GCTGGGCATC AGCTGGCTGG GGCTGCGCTC GCTGAGGGAA 1381 CTGGGCAGTG GACTGGCCCT CATCCACCAT AACACCCGCC TCTGCTTTGT GCACACGGTG 1441 CCCTGGGACC AGCTCTTCCG GAACCCGCAC CAAGCCCTGC TCCACACTGC CAACCGGCCA 1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCG AGGGCACTGC 1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGC TGTGCGCCCG AGGGCACTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG AGGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTTGGCACAG TCTACAAGGG CATCTGGATC	1081						
1261 GACCTTAGCG TCCTCCAGAA CCTGCAAGTA ATCCGGGGAC GAATTCTGCA CAATGGCGCC 1321 TACTCACTGA CCCTGCAAGG GCTGGCATC AGCTGGCTGG GGCTGCGCTC GCTGAGGGAA 1381 CTGGGCAGTG GACTGGCCCT CATCCACCAT AACACCCGCC TCTGCTTTGT GCACACGGCG 1441 CCCTGGGACC AGCTCTTCCG GAACCCGCAC CAAGCCCTGC TCCACACTGC CAACCGGCCA 1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCG AGGGCACTGC 1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTTGGAATCC TCATCTCTGC TGTGGTGGGC 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTTGGCACAG TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTTGGCACAG TCCTGAAAGA GACGGAGCTG							
1321 TACTCACTGA CCCTGCAAGG GCTGGGCATC AGCTGGCTGG GGCTGCGCTC GCTGAGGGAA 1381 CTGGGCAGTG GACTGGCCCT CATCCACCAT AACACCCGCC TCTGCTTTGT GCACACCGGTG 1441 CCCTGGGACC AGCTCTTCCG GAACCCGCAC CAAGCCCTGC TCCACACTGC CAACCGGCCA 1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCG AGGGCACTGC 1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG AAGTGCC CAACCAGGCG CAGATGCCGA TCCTTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTTGGCACAG TCTTACAAGGG CATCTGGATC							
1381 CTGGGCAGTG GACTGGCCCT CATCCACCAT AACACCCGCC TCTGCTTTGT GCACACGGTG 1441 CCCTGGGACC AGCTCTTCCG GAACCCGCAC CAAGCCCTGC TCCACACTGC CAACCCGGCCA 1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCG AGGGCACTGC 1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGACGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGCC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGACCACTG 2101 ACACCGAGTG AGGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
1441 CCCTGGGACC AGCTCTTCCG GAACCCGCAC CAAGCCCTGC TCCACACTGC CAACCGGCCA 1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCG AGGGCACTGC 1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCG AGGGCACTGC 1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC 1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	1441						
1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT 1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	1501						
1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG 1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGCC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	~~~						
1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC 1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	1621	GTGGAGGAAT	GCCGAGTACT	GCAGGGGCTC	CCCAGGGAGT	ATGTGAATGC	CAGACACTGT
1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG 1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGCCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	1681						
1861 GGCACGTGCC AGTCTTGCCC CATCAACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG 1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	1741	L GCTGACCAG	T GTGTGGCCTG	TGCCCACTAT	T AAGGACCCTC	CCTTCTGCGT	GGCCCGCTGC
1921 GGCTGCCCCG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC 1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG 2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC	186	L GGCACGTGC	C AGTCTTGCCC	CATCAACTG	C ACCCACTCCT	GTGTGGACCT	GGATGACAAG
2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG 2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG 2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC							
2221 CCTGATGGGG AGAATGTGAA AATTCCAGTG GCCATCAAAG TGTTGAGGGA AAACACATCC							
	222	1 CCTGATGGG	G AGAATGTGA	A AATTCCAGT	G GCCATCAAAG	TGTTGAGGGA	AAACACATCC

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2281	CCCAAAGCCA	ACAAAGAAAT	CTTAGACGAA	GCATATGTGA	TGGCTGGTGT	GGGCTCCCCA
2341	TATGTCTCCC	GCCTCCTGGG	CATCTGCCTG	ACATCCACGG	TGCAGCTGGT	GACACAGCTT
2401	ATGCCCTATG	GCTGCCTCTT	AGACCATGTC	CGAGAAAACC	GCGGACGCCT	GGGCTCCCAG
2461	GACCTGCTGA	ACTGGTGTAT	GCAGATTGCC	AAGGGGATGA	GCTACCTGGA	GGATGTGCGG
2521	CTCGTACACA	GGGACTTGGC	TGCTCGGAAC	GTGCTGGTCA	AGAGTCCCAA	CCATGTCAAA
2581	ATTACAGACT	TTGGGCTGGC	TCGGCTGCTG	GACATTGACG	AGACAGAGTA	CCATGCAGAT
2641	GGGGGCAAGG	TGCCCATCAA	GTGGATGGCG	CTGGAGTCCA	TTCTCCGACG	GCGGTTCACC
2701	CACCAGAGTG	ATGTGTGGAG	TTATGGTGTG	ACTGTGTGGG	AGCTGATGAC	TTTTGGGGCC
2761	AAACCTTACG	ATGGGATCCC	AGCCCGGGAG	ATCCCTGACC	TGCTGGAAAA	GGGGGAGCGG
2821	CTGCCCCAGC	CCCCCATCTG	CACCATTGAT	GTCTACATGA	TCATGGTCAA	ATGTTGGATG
2881	ATTGACTCTG	AATGTCGGCC	GAGATTCCGG	GAGTTGGTGT	CGGAATTCTC	CCGCATGGCC
2941	AGGGACCCCC	AGCGCTTTGT	GGTCATCCAG	AATGAGGACT	TGGGCCCAGC	CAGTCCCTTG
3001	GACAGCACCT	TCTACCGCTC	ACTGCTGGAG	GACGATGACA	TGGGGGACCT	GGTGGATGCT
3061	GAGGAGTATC	TGGTACCCCA	GCAGGGCTTC	TTCTGTCCAG	ACCCTGCCCC	GGGCACTGGG
3121	GGCATGGTCC	ACCACAGGCA	CCGCAGCTCA	TCTACCAGGA	GTGGCGGTGG	GGACCTGACG
3181	CTAGGGCTGG	AGCCCTCTGA	AGAGGAGGCC	CCCAGGTCTC	CACGGGCACC	CTCCGAAGGG
3241	ACTGGCTCTG	ATGTATTTGA	TGGTGACCTA	GGAATGGGGG	CAGCCAAGGG	GCTGCAAAGC
3301	CTCCCCGCAC	ATGACCCCAG	CCCTCTACAG	CGGTACAGTG	AGGACCCCAC	GGTACCCCTG
3361	CCTTCTGAGA	CTGACGGCTA	CGTTGCCCCC	CTGACCTGCA	GTCCCCAGCC	CGAATATGTG
3421	AACCAGCCAG	ATGTTCGGCC	ACAGCCCCCT	TCGCCCCAAG	AGGGCCCTCT	GTCTCCTGCC
3481	CGACCTACTG	GTGCCACTCT	GGAAAGGCCC	AAGACTCTCT	CCCCAGGGAA	GAATGGGGTT
3541	GTCAAAGACG	TTTTTGCCTT	TGGGGGTGCT	GTGGAGAACC	CCGAGTACTT	GGCACCCCGG
3601	GGAGGAGCTG	CCCCTCAGCC	CCACCTTCCT	CCTGCCTTCA	GCCCAGCCTT	CGACAACCTC
3661	TATTACTGGG	ACCAGGACCC	ATCAGAGCGG	GGGGCTCCAC	CTAGCACCTT	CAAAGGGACA
3721	CCTACGGCAG	AGAACCCAGA	GTACCTGGGT	CTGGACGTGC	CAGTGTGA (S	SEQ ID NO:1)

FIG.1B

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Predicted Amino Acid Sequence of First Rhesus Her2/Neu Protein (SEQ ID NO:2)

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1 MELAAWYRWG LLLALLPPGA AGTQVCTGTD MKLRLPASPE THLDMLRHLY QGCQVVQGNL
 61 ELTYLPTNAS LSFLQDIQEV QGYVLIAHNQ VRQVPLQRLR IVRGTQLFED NYALAVLDNG
121 DLLNNTTPVT GASPGGLREL QLRSLTEILK GGVLIQRNPQ LCYQDTILWK DIFHKNNQLA
181 LTLIDTNRSR ACHPCSPVCK GSRCWGESSE DCQSLTRTVC AGGCARCKGP LPTDCCHEQC
241 AAGCTGPKHS DCLACLHFNH SGICELHCPA LVTYNTDTFE SMPNPEGRYT FGASCVTACP
301 YNYLSTDVGS CTLVCPLHNQ EVTAEDGTQR CEKCSKPCAR VCYGLGMEHL REVRAVTSAN
361 IQEFAGCKKI FGSLAFLPES FDGDPASNTA PLQPEQLRVF ETLEEITGYL YISAWPDSLP
421 DLSVLQNLQV IRGRILHNGA YSLTLQGLGI SWLGLRSLRE LGSGLALIHH NTRLCFVHTV
481 PWDQLFRNPH QALLHTANRP EDECVGEGLA CHQLCARGHC WGPGPTQCVN CSQFLRGQEC
541 VEECRVLQGL PREYVNARHC LPCHPECQPQ NGSVTCFGPE ADQCVACAHY KDPPFCVARC
601 PSGVKPDLSY MPIWKFPDEE GTCQSCPINC THSCVDLDDK GCPAEQRASP LTSIISAVVG
661 ILLVVVLGVV FGILIKRRQQ KIRKYTMRRL LQETELVEPL TPSGAMPNQA QMRILKETEL
721 RKVKVLGSGA FGTVYKGIWI PDGENVKIPV AIKVLRENTS PKANKEILDE AYVMAGVGSP
781 YVSRLLGICL TSTVQLVTQL MPYGCLLDHV RENRGRLGSQ DLLNWCMQIA KGMSYLEDVR
841 LVHRDLAARN VLVKSPNHVK ITDFGLARLL DIDETEYHAD GGKVPIKWMA LESILRRRFT
901 HQSDVWSYGV TVWELMTFGA KPYDGIPARE IPDLLEKGER LPQPPICTID VYMIMVKCWM
961 IDSECRPRFR ELVSEFSRMA RDPQRFVVIQ NEDLGPASPL DSTFYRSLLE DDDMGDLVDA
1021 EEYLVPQQGF FCPDPAPGTG GMVHHRHRSS STRSGGGDLT LGLEPSEEEA PRSPRAPSEG
1081 TGSDVFDGDL GMGAAKGLQS LPAHDPSPLQ RYSEDPTVPL PSETDGYVAP LTCSPQPEYV
1141 NQPDVRPQPP SPQEGPLSPA RPTGATLERP KTLSPGKNGV VKDVFAFGGA VENPEYLAPR
1201 GGAAPQPHLP PAFSPAFDNL YYWDQDPSER GAPPSTFKGT PTAENPEYLG LDVPV*
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FIG.2

Oligonucleotide Primers Spanning Rhesus Her2/neu Gene

		,	
Forward	Sequence	Keverse	
(01-)-(02-)	ASSCATGGGGCCCGCA (SEQ 10 NO:3)	96-79	CTTCATGTGTGGGGGGT (SEQ ID NO:20)
(-22)-(-1)	GCCCCCACCCCCACTGACCACC (SEQ ID NO:21)	431-409	CTTCSARCTGCAGCTCCCCCAG (SEQ ID NO:22)
1-25	ATGGAGCTGGCGGCTTGTGCCCTT (SEQ 10	812-787	ACCCCCCCCCCCCCCCCACAT (SEQ 1D NO:4)
	NO:23)		
36-6/	ACCISCACACACATGAAG (SEQ 10 NO:24)	1115-1096	CCAAACATCTTCTTGCAGCC (SEQ 1D NO:6)
409-431	CTGCGGGGAGCTGCGAGC (SEQ ID NO:5)	1370-1352	GAGCCCAGCCCCAGCCAGC (SEQ ID NO:8)
787-812	ATCTGTGAGCTGCACAGCCT (SEQ 10 NO.7)	1583-1558	CACTESESTEGSECCTEGSACCCCASCA (SEQ 1D NO:25)
1096-1115	GCCICCARGAGATCTTICE (SEQ 10 NO:9)	1895-1876	IGGSTGCASTTGATGGGGCA (SEQ ID NO:10)
1352-1370	CCTCCCTCCCCCCCCC (SEQ 10 NO:27)	2183-2161	
1558-1583	TECTGOSCITCAGOCCAGOCAGIG (SEQ 10	2222-2200	GESATCEAGATGEECTTGTAGAC (SEQ 10 NO:28)
	NO:12)		
1876-1895	TOCCCATCAACTGCACCCA (SEQ 10 NO:29)	2277-K753A-2239	TGTGTTTTCCCTCAACACGCGATGGCCACTGGAATTTT (SEQ 1D NO:15)
2161-2183	AGGAGGTGAGCTGCTTGCATC (SEQ 1B NO:31)	2378-2356	GIESATGTCAGGCAGATGCCCAG (SEQ 1D NO:30)
2200-2222	GTCTACAAGGGCATCTGGATCCC (SEQ 10 NO:33)	2768-2743	TARGETTICGCCCCAAAAGTCATCAG (SEQ ID NO:32)
2239-K753A 2277	AAAATTCCAGTGGCCATGGCCGTGTTGAGGGAAAACACA	2798-2776	TCAGGGATCTCCCGGGGGAT (SEQ ID NO:13)
9746_9478	CHASSCALFIGGETGACATOCAC (SEG 10 NO:17)	3410-3388	GECTORGECTECAGETCAGECE (SEQ 1D NO: 34)
2743-2768	CTGATGACTTTTGGGGCCAAACCTTA (SEQ 10	Sal1_3768-3746	GOOSTOCACTITACATGGCACSTOCASACOCA (SEQ 10
; ;	NO:35}		NO:19}
2776-2798	ATCCCACOCCSCACATCCCTGA (SEQ 10 NO:37)	3791-3770	TICTECKSCACTTECKCCTTCTGS (SEQ 10 NO: 36)
3388-34102	COCCIGACCIGCACCCCCACCC (SEQ ID NO:39)	3885-3869	rescreettococtega (seq 10 no:38)
1621-1644	GTGGAGGAATGCCGAGTACTGCAG (SEQ 10 NO:14)	4166-4145	GETTICAGGGACACICICIGAA (SEQ ID NO:18)
Pinel_Swal_RBS_1-16	( –		
	GGCCT (SEQ 10 NO:11)		

RI—PCR Primers and Clones Used to Construct Full—Length rhHER2/neu Clone.

Reverse   Reverse		Oligonucleotide Primer	lide Primer	Clone
AGCCATGGGGCCCGCAC (SEQ ID NO:3)  CTGCGGCAGCTGCAGC (SEQ ID NO:5)  ATCTGTGAGCTGCACTCCAAG (SEQ ID NO:5)  NO:7)  GCTGCAAGAAGATCTTTGG (SEQ ID NO:9)  CCAGTTTAAACATTTAAATGCCGCCACCATGCAGCTGG  CCAGTTTAAACATTTAAATGCCCCCACCATGCAGCTGG  CCAGTTTAAACATTTAAATGCCCCCACCCATGCAGCCTGG  CCAGTTTAAACATTTAAATGCCCCACCCATGCAGCCAGCC	Rxn.#	Forward	Reverse	
CTGGGGGGGCTGCCTTCGAGC (SEQ 1D NO:5)  ATCTGTGAGCTGCCCTCCCAGCCCT (SEQ 1D NO:7)  NO:7)  GGCTGCAAGAAGATCTTTGG (SEQ 1D NO:9)  CCAGTTTAAACATTTAAATGCCGCCACCATGGAGCTGG  CGGCCT (SEQ 1D NO:11)  TGCTGGGGTCCAGGGCCCACCCAGTG (SEQ 1D NO:12)  CTGGGGGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)  AAAATTCCAGTGCCCATCGCCGTTTGAGGGAAACAC  A (SEQ 1D NO:16)  CTGGGCATCTGCCTGACTCCAG (SEQ 1D NO:17)  CTGGGCATCTGCCTGACTCCAG (SEQ 1D NO:17)  CTGGGCATCTGCCTGACTGCCAG (SEQ 1D NO:14)  NO:14)  O GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)  NO:14)	-	AGCCATGGGCCCGGAGCCGCA	AGGCCTGGCCAGTGCAGCTCACAGAT (SEQ ID NO:4)	#1_BS_(-30)-812.A1
ATCTGTGAGCTGCCCCAGCCCT (SEQ 1D N0:7)  (GCTGCAAGAAGATCTTTGG (SEQ 1D N0:9)  (CCAGTTTAAACATTTAAATGCCGCCACCATGGAGCTGG  (CCAGTTTAAACATTTAAATGCCGCCACCATGGAGCTGG  (CCAGTTTAAACATTTAAATGCCGCCACCATGGAGCTGG  (CCAGTTTAAACATTTAAATGCCGCCACCCATGGAGCTGG  (CCAGTTTAAACATTTAAATGCCGCCATGGCCACCCATGGCCACTGGCCATGCCCATGCCCACTGGCCATGGCCATGCCCATGCCCAGTTGAGGCAAAACAC  (A SEQ 1D N0:16)  (CTGCGCAATGCCCATCGCCATGGCGGAAACAC  (CTGCGCATCTGCCTGACATGCCCAGTACTGCAG (SEQ 1D  (CTGCGCAATGCCCAGTACTGCAG (SEQ 1D  (CTGCGCAATGCCCAGTACTGCAG (SEQ 1D  (CTGCAATGCCCAGTACTGCAG (SEQ 1D  (CTGCAATGCCCAGTACTGCCAG (SEQ 1D  (CTGCAATGCCCAGTACTGCCAG (SEQ 1D  (CTGCAATGCCCAATGCCCAGTACTGCCAG (SEQ 1D  (CTGCAATGCCCAATGCCCAGTACTGCCAG (SEQ 1D  (CTGCAATGCCCAATGCCCAGTACTGCCAG (SEQ 1D  (CTGCAATGCCCAATGCCCAATGCCCAGTACTGCCAG (SEQ 1D  (CTGCAATGCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCCAATGCCAATGCCCAATGCCCAATAATGCCAATAATGCCAATGCCAATAATGCCAATAATGCCAATAATGCCAATAATAATAATAATAATAAA	6	CTGGGGGGGGCTCGAAG (SEQ ID NO:5)	CCAAAGATCTTCTTGCAGCC (SEQ ID NO:6)	#1_CR_409_1115.2
GGCTGCAAGAAGATCTTTGG (SEQ 1D NO:9)  CCAGTTTAAACATTTAAATGCCGCCACCATGGAGCTGG CGGCCT (SEQ 1D NO:11)  TGCTGGGGTCCAGGGCCCACCCAGTG (SEQ 1D NO:12)  CTGGAGCAATGCCGAGTACTGCAG (SEQ 1D NO:14)  AAAATTCCAGTGCCCATCGCCGTGTTGAGGGAAACAC A (SEQ 1D NO:16)  CTGGCCATCTGCCTGACTCCCAG (SEQ 1D NO:14)  O GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)  O GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)	2	ATCTGTGAGCTGCACTGCCCAGCCCT (SEQ 10	GAGOGCAGCCCAGCCAGC (SEQ ID NO:8)	#1_CR_787_1370.10
CCAGITTAAACATTTAAATGCCGCCACCATGGAGCTGG CGGCCT (SEQ ID NO:11) TGCTGGGGTCCAGGGCCCCCATG (SEQ ID NO:12) GTGGAGCAATGCCGAGTACTGCAG (SEQ ID NO:14) AAAATTCCAGTGGCCATCCCCGTGTTGAGGGAAACAC A (SEQ ID NO:16) CTGGCCATCTGCCTGACTCCCC (SEQ ID NO:17) CTGGCATCTGCCTGACTCCCA (SEQ ID NO:17) CTGGCAATGCCGAGTACTGCAG (SEQ ID NO:14) 0 GTGCAGCAATGCCGAGTACTGCAG (SEQ ID NO:14)	4	AAGAAGATCTTTGG (	TGGGTGCAGTTGATGGGGCA (SEQ ID NO:10)	#1_BS_1096_1895.11
CGGCCT (SEQ ID NO:11)  TGCTGGGGTCCAGGGCCCACCGTG (SEQ ID NO:12)  GTGCAGCAATGCCGAGTACTGCAG (SEQ ID NO:14)  AAAATTCCAGTGGCCATCGCCGTGTTGAGGGAAACAC A (SEQ ID NO:16)  CTGGCCATCTGCCTGACATCCCAG (SEQ ID NO:17)  GTGCAGCAATGCCGAGTACTGCAG (SEQ ID NO:14)  0 GTGCAGCAATGCCGAGTACTGCAG (SEQ ID NO:14)	. 2	CCAGTTTAAACATTTAAATGCCGCCACCATGGAGCTGG	TGGGTGCAGTTGATGGGGCA (SEQ ID NO:10)	#1_CR_1-1895.7(-)
TGCTGGGGTCCAGGCCCACCCAGTG (SEQ ID NO:12)  GTGGAGGAATGCCGAGTACTGCAG (SEQ ID NO:14)  AAAATTCCAGTGGCCATCGCCGTGTTGAGGGAAACAC AAAATTCCAGTGCCCATCGCCGTGTTGAGGGAAACAC AAAATTCCAGTGCCCATCGCCGTGTTGAGGGAAACAC (SEQ ID NO:17)  GTGGAGGAATGCCGAGTACTGCAG (SEQ ID NO:14)  0 GTGGAGGAATGCCGAGTACTGCAG (SEQ ID NO:14)  NO:14)		CGCCCT (SEQ ID NO:11)		(0000 030)
NO:12) GTGGAGGAATGCCGAGTACTGCAG (SEQ ID NO:14) AAAATTCCAGTGGCCATCGCCGTGTTGAGGGAAACAC A (SEQ ID NO:16) CTGGCCATCTGCCTGACATCCCAC (SEQ ID NO:17) CTGGCATCTGCCTGACATCCCAC (SEQ ID NO:14) 0 GTGCAGGAATGCCGAGTACTGCAG (SEQ ID NO:14)	9	TCCTGGGGTCCAGGCCCACCAGTG (SEQ ID	TCAGGGATCTCCCGGGCTGGGAT (SEQ ID NO:13)	Not Cloned (1538-2/98)
GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D N0:14)  AAAATTCCAGTGGCCATCGCCGTGTTGAGGGAAACAC A (SEQ 1D N0:16).  CTGGGCATCTGCCTGACATCCAC (SEQ 1D N0:17)  GTGGAGGAATGCCGACATCTGCAG (SEQ 1D N0:14)  0 GTGCAGGAATGCCGAGTACTGCAG (SEQ 1D N0:14)		N0:12)		0 LEGO 1001 GO !!
NO:14)  AAAATTCCAGTGCCCATCGCCGTGTTGAGGGAAACAC A (SEQ 1D NO:16).  CTGGCCATCTGCCTGACATCCCAC (SEQ 1D NO:17)  GTGCAGGAATGCCCAGTACTGCAG (SEQ 1D NO:14)  O GTGCAGGAATGCCCAGTACTGCAG (SEQ 1D NO:14)	7	GTGGAGGAATGCCGAGTACTGCAG (SEQ ID	TGTGTTTTCCCTCAACACGCCATGCCCACTGGAATIII	#1_CR_1621-72//.2
AAAATTCCAGTGGCCATCGCCGTGTTGAGGGAAAACAC A (SEQ ID NO:16) CTGGGCATCTGCCTGACATCCAC (SEQ ID NO:17) CTGGCAATGCCCAGTACTGCAC (SEQ ID NO:14) 0 GTGCAGGAATGCCCAGTACTGCAC (SEQ ID NO:14)		NO:14)	(SEQ ID NO:15)	
A (SEQ ID NO:16). CTGGGCATCTGCCTGACATCCAC (SEQ ID NO:17) 0 GTGCAGCAATGCCCAGTACTGCAG (SEQ ID NO:14) 0 GTGCAGCAATGCCCAGTACTGCAG (SEQ ID NO:14)	<sub>∞</sub>	AAAATTCCAGTGGCCATGGCGGTGTTGAGGGAAAACAC	TCAGGGATCTCCCGGGCTGGGAT (SEQ ID NO:13)	#1_CR_2239-2/98.4
CTGGGCATCTGCCTGACATCCAC (SEQ 1D NO:17)  0 GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)  0 GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)		A (SEQ ID NO:16).		
GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14) GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)	6	CTGGGCATCTGCCTGACATCCAC (SEQ ID NO:17)	GGTTTCAGGGACAGTCTCTGAA (SEQ ID NO:18)	#1_CR_2356-4166.2
NO:14) GTGGAGGAATGCCGAGTACTGCAG (SEQ ID NO:14)	9	GTGGAGGAATGCCGAGTACTGCAG (SEQ ID	GCGSTCSACTTTACATGGACAGTCCAGACCCA (SEQ	#1_CR_1621-3768.8(+)
GTGGAGGAATGCCGAGTACTGCAG (SEQ 1D NO:14)		NO:14)	ID NO:19)	
	9	GTGGAGGAATGCCGAGTACTGCAG (SEQ ID	GCCGTCCACTTTACATGCACACTCCAGACCCA (SEQ	#1_CR_1621-3768.12(+)
		NO:14)	(ID NO:19)	

FIG. 4

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## Nucleotide Sequence of Second Rhesus HER2/Neu

```
1 ATGGAGCTGG CGGCCTGGTA CCGCTGGGGG CTCCTCCTCG CCCTCTTGCC CCCCGGAGCT
 61 GCGGGCACCC AAGTGTGCAC CGGCACAGAC ATGAAGCTGC GGCTCCCTGC CAGTCCCGAG
121 ACCCACCTGG ACATGCTCCG CCACCTCTAC CAGGGCTGCC AGGTGGTGCA GGGTAACCTG
181 GAACTCACCT ACCTGCCCAC CAATGCCAGC CTCTCCTTCC TGCAGGATAT CCAGGAGGTG
241 CAGGGCTACG TGCTCATCGC TCACAACCAA GTGAGGCAGG TCCCACTGCA GAGGCTGCGG
301 ATTGTGCGAG GCACCCAGCT CTTTGAGGAC AACTATGCCC TGGCCGTGCT AGACAATGGA
361 GACCCGCTGA ACAATACCAC CCCTGTCACA GGGGCCTCCC CAGGAGGCCT GCGGGAGCTG
421 CAGCTTCGAA GCCTCACAGA GATCTTGAAA GGAGGGGTCT TGATCCAGCG GAACCCCCAG
481 CTCTGCTACC AGGACACGAT TTTGTGGAAG GACATCTTCC ATAAGAACAA CCAGCTGGCT
541 CTCACACTGA TCGACACCAA CCGCTCTCGG GCCTGCCACC CCTGTTCTCC AGTGTGTAAG
601 GGCTCCCGCT GCTGGGGAGA GAGTTCTGAG GATTGTCAGA GCCTGACGCG CACTGTCTGT
661 GCCGGTGGCT GTGCCCGCTG CAAGGGGCCA CTGCCCACTG ACTGCTGCCA TGAGCAGTGT
721 GCTGCCGGCT GCACGGGCCC CAAGCACTCT GACTGCCTGG CCTGCCTCCA CTTCAACCAC
781 AGCGGCATCT GTGARCTGCA CTGCCCAGCC CTGGTCACCT ACAACACAGA CACCTTTGAG
841 TCCATGCCCA ACCCCGAGGG CCGGTATACA TTCGGCGCCA GCTGTGTGAC TGCCTGTCCC
901 TACAACTACC TTTCTACGGA CGTGGGATCC TGCACCCTCG TCTGCCCCCCT GCACAACCAA
961 GAGGTGACAG CGGAGGACGG AACACAGCGA TGTGAGAAGT GCAGCAAGCC CTGTGCCCGA
1021 GTGTGCTATG GTCTGGGCAT GGAGCACTTG CGAGAGGTGA GGGCGGTCAC CAGTGCCAAT
1081 ATCCAGGAGT TTGCTGGCTG CAAGAAGATC TTTGGGAGYT TGGCATTTCT GCCAGAGAGC
1141 TTTGATGGCG ACCCAGCCTC CAACACCGCC CCGCTTCAGC CGGAGCAGCT CCGAGTGTTT
1201 GAGACTCTGG AAGAGATCAC AGGTTACCTA TACATCTCAG CATGGCCAGA CAGCCTGCCT
1261 GACCTTAGCG TCCTCCAGAA CCTGCAAGTA ATCCGGGGAC GAATTCTGCA CAATGGCGCC
1321 TACTCACTGA CCCTGCAAGG GCTGGGCATC AGCTGGCTGG GGCTGCGCTC GCTGAGGGAA
1381 CTGGGCAGTG GACTGGCCCT CATCCACCAT AACACCCGCC TCTGCTTTGT GCACACGGTG
1441 CCCTGGGACC AGCTCTTCCG GAACCCGCAC CAAGCCCTGC TCCACACTGC CAACCGGCCA
1501 GAGGACGAGT GTGTGGGCGA GGGCCTGGCC TGCCACCAGC TGTGCGCCCR AGGGCACTGC
1561 TGGGGTCCAG GGCCCACCCA GTGTGTCAAC TGCAGCCAGT TCCTTCGGGG CCAGGAGTGC
1621 GTGGAGGAAT GCCGAGTACT GCAGGGGCTC CCCAGGGAGT ATGTGAATGC CAGACACTGT
1681 TTGCCGTGCC ACCCTGAGTG TCAGCCCCAG AATGGCTCAG TGACATGTTT TGGACCGGAG
1741 GCTGACCAGT GTGTGGCCTG TGCCCACTAT AAGGACCCTC CCTTCTGCGT GGCCCGCTGC
1801 CCCAGCGGTG TGAAACCTGA CCTCTCCTAC ATGCCCATCT GGAAGTTTCC AGATGAGGAG
1861 GGCACGTGCC AGCCTTGCCC CATCAACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG
1921 GGCTGCCCG CCGAGCAGAR AGCCAGCCCT CTGACGTCCA TCATCTCTGC TGTGGTGGGC
1981 ATTCTGCTGG TCGTGGTCTT GGGGGTGGTC TTTGGAATCC TCATCAAGCG ACGGCAGCAG
2041 AAGATCCGGA AGTACACGAT GCGGAGGCTG CTGCAGGAAA CGGAGCTGGT GGAGCCACTG
2101 ACACCGAGTG GAGCGATGCC CAACCAGGCG CAGATGCGGA TCCTGAAAGA GACGGAGCTG
2161 AGGAAGGTGA AGGTGCTTGG ATCTGGAGCT TTTGGCACAG TCTACAAGGG CATCTGGATC
2221 CCTGATGGGG AGAATGTGAA AATTCCAGTG GCCATCAAAG TGTTGAGGGA AAACACATCC
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2281 CCCAAAGCCA ACAAAGAA	AT CTTAGACGAA	GCATATGTGA	TGGCTGGTGT	GGGCTCCCCA
2341 TATGTCTCCC GCCTCCTC				
2401 ATGCCCTATG GCTGCCTC	CTT AGACCATGTC	CGAGAAAACC	GCGGACGCCT	GGGCTCCCAG
2461 GACCTGCTGA ACTGGTGT				
2522 CTCGTACACA GGGACTTO	GC TGCTCGGAAC	GTGCTGGTCA	AGAGTCCCAA	CCATGTCAAA
2581 ATTACAGACT TTGGGCTG				
2641 GGGGCAAGG TGCCCATO				
2701 CACCAGAGTG ATGTGTGG				
2761 AAACCTTACG ATGGGAT	CC AGCCCGGGAG	ATCCCTGACC	TGCTGGAAAA	GGGGGAGCGG
2821 CTGCCCCAGC CCCCCATO	CTG CACCATTGAT	GTCTACATGA	TCATGGTCAA	ATGTTGGATG
2881 ATTGACTCTG AATGTCGG				
2941 AGGGACCCCC AGCGCTTT				
3001 GACAGCACCT TCTACCG				
3061 GAGGAGTATC TGGTACCO				
3121 GGCATGGTCC ACCACAGG				
3181 CTAGGGCTGG AGCCCTCT				
3241 ACTGGCTCTG ATGTATT				
3301 CTCCCCGCAC ATGACCCC				
3361 CCTTCTGAGA CTGACGG	CTA CGTTGCCCCC	CTGACCTGCA	GYCCCCAGCC	CGAATATGTG
3421 AACCAGCCAG ATGTTCGG				
3481 CGACCTACTG GTGCCACT	TCT GGAAAGGCCC	AAGACTCTCT	CCCCAGGGAA	GAATGGGGTT
3541 GTCAAAGACG TTTTTGC				
3601 GGAGGAGCTG CCCCTCAG				
3661 TATTACTGGG ACCAGGAG				
3721 CCTACGGCAG AGAACCCA	GA GTACCTGGGT	CTGGACGTGC	CAGTGTGA (S	SEQ ID NO:40)

FIG.5B

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Predicted Amino Acid Sequence of Second Rhesus Her2/Neu Protein

```
1 MELAAWYRWG LLLALLPPGA AGTQVCTGTD MKLRLPASPE THLDMLRHLY QGCQVVQGNL
 61 ELTYLPTNAS LSFLQDIQEV QGYVLIAHNQ VRQVPLQRLR IVRGTQLFED NYALAVLDNG
121 DPLNNTTPVT GASPGGLREL QLRSLTEILK GGVLIQRNPQ LCYQDTILWK DIFHKNNQLA
181 LTLIDTNRSR ACHPCSPVCK GSRCWGESSE DCQSLTRTVC AGGCARCKGP LPTDCCHEQC
241 AAGCTGPKHS DCLACLHFNH SGICELHCPA LVTYNTDTFE SMPNPEGRYT FGASCVTACP
301 YNYLSTDVGS CTLVCPLHNQ EVTAEDGTQR CEKCSKPCAR VCYGLGMEHL REVRAVTSAN
361 IQEFAGCKKI FGSLAFLPES FDGDPASNTA PLQPEQLRVF ETLEEITGYL YISAWPDSLP
421 DLSVLQNLQV IRGRILHNGA YSLTLQGLGI SWLGLRSLRE LGSGLALIHH NTRLCFVHTV
481 PWDQLFRNPH QALLHTANRP EDECVGEGLA CHQLCAXGHC WGPGPTQCVN CSQFLRGQEC
541 VEECRVLQGL PREYVNARHC LPCHPECQPQ NGSVTCFGPE ADQCVACAHY KDPPFCVARC
601 PSGVKPDLSY MPIWKFPDEE GTCQPCPINC THSCVDLDDK GCPAEQXASP LTSIISAVVG
661 ILLVVVLGVV FGILIKRRQQ KIRKYTMRRL LQETELVEPL TPSGAMPNQA QMRILKETEL
721 RKVKVLGSGA FGTVYKGIWI PDGENVKIPV AIKVLRENTS PKANKEILDE AYVMAGVGSP
781 YVSRLLGICL TSTVQLVTQL MPYGCLLDHV RENRGRLGSQ DLLNWCMQIA KGMSYLEDVR
841 LVHRDLAARN VLVKSPNHVK ITDFGLARLL DIDETEYHAD GGKVPIKWMA LESILRRRFT
901 HQSDVWSYGV TVWELMTFGA KPYDGIPARE IPDLLEKGER LPQPPICTID VYMIMVKCWM
961 IDSECRPRFR ELVSEFSRMA RDPQRFVVIQ NEDLGPASPL DSTFYRSLLE DDDMGDLVDA
1021 EEYLVPQQGF FCPDPAPGTG GMVHHRHRSS STRSGGGDLT LGLEPSEEEA PRSPXAPSEG
1081 TGSDVFDGDL GMGAAKGLQS LPAHDPSPLQ RYSEDPTVPL PSETDGYVAP LTCSPQPEYV
1141 NQPDVRPQPP SPQEGPLSPA RPTGATLERP KTLSPGKNGV VKDVFAFGGA VENPEYLAPR
1201 GGAAPQPHLP PAFSPAFDNL YYWDQDPSER GAPPSTFKGT PTAENPEYLG LDVPV*
(SEQ ID NO:41)
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FIG.6

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# MUTATIONS IN RHESUS HER2/neu NUCLEOTIDE SEQUENCE

				1	<del></del> 1
POSITION	RhHER2#1		POSITION	RhHER2#2	
365	2 CLONES	C TAG	365	2 CLONES	C C G
		Fig. Co.		L	PRO
				1 4 0 0 0	To 4 Ko1
795	3 CLONES	G A FG	795	1 CLONE	G A G
	0.01.01.00	DE		O CLONES	CAPA
	2 CLONES	G A A		2 CLONES	G A A
L		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	L	<u> </u>	P. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
1119	2 CLONES	IA G KC3	1119	3 CLONES	TA GET
1119	2 OLONES	A G FC ≥ S ≥ S ≥ S ≥ S ≥ S ≥ S ≥ S ≥ S ≥ S ≥	)	O OLONEO	SS.
]		1222	]	2 CLONES	AGEC
!					A G C
1550	3 CLONES	CEGAA	1550	2 CLONES	CFAIA
1		SS R SS			530 Q 1000
				3 CLONES	CFGIA
		لـــــــــــــــــــــــــــــــــــــ		<u></u>	深R%数
1873	6 CLONES	FTAC T	1873	11 CLONES	KUL T
10/3	O CLONES	TIC T	1073	I I OLONES	CCCT
L	<u> </u>	1344 0414 54	<u> </u>	<del> </del>	Particular 1 - 1 - 1 - 1 - 1
1940	2 CLONES	AFGIA	1940	1 3 CLONES	TAFAJA
1310	2 0201120	A EG A A	1		K.5.7
1		111111111111111111111111111111111111111		3 CLONES	A GA
			L	<u> </u>	SA RESS
					1000
3224	4 CLONES	CFGAG R	3224	5 CLONES	C G1G
		STATE OF THE PERSON NAMED IN		7 CLONES	CEALO
1	}			3 CLONES	CFAIG Q
	L		L		Keer Missel
7402	1 2 CLONES	IA C ETA	3402	2 CLONES	IA G KC
3402	Z CLUNES	A G I	J40Z	2 CLUIVES	A G FC
		3,5,0,00		6 CLONES	A G T
1		\ \ \ \ \		0 OLONES	SES SES
<u> </u>			<del></del>		

FIG.7